From:	Jay Field
To:	Eric Blischke/R10/USEPA/US@EPA
Cc:	Robert Gensemer; Burt Shephard/R10/USEPA/US@EPA; Chip Humphrey/R10/USEPA/US@EPA; Joe Goulet/R10/USEPA/US@EPA; Robert Neely
Subject:	Re: Summary of Sediment Bioassay Interpretation Resolution
Date:	07/14/2009 12:18 PM

Eric,
Regarding number 4): It does matter, since it gives more weight to two of the stations in the reference envelope. You could include both but give them a weight of 1/2, if your curve fitting package allows weighting. Helping the curve fitting procedure is kind of irrelevant if the distribution is skewed by including two samples twice.
Jay

Blischke.Eric@epamail.epa.gov wrote:
> Bob, thanks for the quick response. I have a few questions/comments:
>
> Regarding number 2), do we understand why the biomass values don't
> match. If the control normalization was done correctly and there were
> no reporting errors,could there be a difference in how total biomass was
> reported?
> Regarding number 3), I will make sure that I specify survivorship in my
> email.
> Regarding number 4), it seems we did not specify whether to pool or to
> handle to duplicates as individual sample results when calculating the
> reference envelope. My question is two-fold - 1) does it matter? and 2)
> if we include the duplicates as individual samples, could this help our
> curve fitting procedure because we now have an additional one or two
> samples?
> Regarding number 6) Burt and I discussed this. He seemed to think that
> it is more valid statistically to fit the entire curve rather than the
> lower end due to the small number of samples at the lower end of the
> distribution. My original thought was along the lines of yours but Burt
> convinced me otherwise. We can revisit this though.
>
> Once I get some additional feedback, I will finalize the email and send
> to John Toll and Bob Wyatt.
>
> Thanks, Eric
>
>
>
> Robert Gensemer
> <rgensemer@param
> etrix.com> To
> Eric Blischke/R10/USEPA/US@EPA,
> 07/13/2009 08:34 Burt Shephard/R10/USEPA/US@EPA,
> PM "jay.field@noaa.gov"
> <jay.field@noaa.gov>, Joe
> Goulet/R10/USEPA/US@EPA
> cc
> Chip Humphrey/R10/USEPA/US@EPA
> Subject
> RE: Summary of Sediment Bioassay
> Interpretation Resolution
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> Eric: A few observations from my perspective:
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> 2) The control-normalization looks correct for biomass, but if I recall
> (I don't have my files with me at the moment) that LWG's biomass values
> for individual stations did not quite match values that Jay derived for
> table RE-1.
> 3) You have the control normalization correct (test/control) but we need
> to be careful to recommend use of survivorship, not mortality, to be
> fully consistent with our guidance and numeric examples. I realize Table
> 2-1 used mortality, but we have been very consistent all along that we
> need to use survivorship, and from a recent call with Burt, Don McD.
> agrees that control-normalized survivorship is the correct value to use,
> not ctrl-norm mortality. Yes, they relate directly (or should I say,
> inversely) to one another, but the 5th percentile calculation could be
> different using one vs. the other, so we need to be consistent, and use
> survivorship.
> 4) I could not find any explicit guidance regarding the duplicate RE
> samples. Its not in the McDonald report that I can find, and I don't
> think we went into this level of detail in the problem formulation. It
> may be one of those things that just seemed very obvious to all of us,
> and so never felt the need to explicitely direct it. Actually, it may
> have only come up, to my recollection, during our own RE calculations in
> March. So table RE-1 definitely reflects this approach, although I don't
> think it was spelled out in the text.
> 6) I agree with your summary here, except to say that we need to not
> just chose the best overall curve fit, but particularly in the case of
> Hyalella biomass, we need a curve that fits the lower tail (i.e., 5th
> %ile) of the distribution best. For the other three endpoints, this is

> probably not an issue (i.e., best fit is also best 5th %ile fit). But
> for Hyl biomass, we need to think more carefully about what distribution
> fits at the lower tail of the distribution. I think this is a valid
> approach that makes the best out of the available data. LWG's curve fit
> created a 5th %ile value that was quite a bit lower than the empirical
> numbers; I do not think that was the most appropriate representation of
> the data.
>
> Bob
>
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>
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>
> þ Before printing, please think green.
>
>
> From: Blischke.Eric@epamail.epa.gov [Blischke.Eric@epamail.epa.gov]
> Sent: Monday, July 13, 2009 5:02 PM
> To: Robert Gensemer; Shephard.Burt@epamail.epa.gov; jay.field@noaa.gov;
> Goulet.Joe@epamail.epa.gov
> Cc: Humphrey.Chip@epamail.epa.gov
> Subject: Summary of Sediment Bioassay Interpretation Resolution
>
>
> As you are aware, we have been discussing some of the details of the
> LWG's interpretation of the Portland Harbor sediment bioassay results.
> Some elements of the interpretation were discussed during a conference
> call on Thursday, June 18, 2009.
>
> Here is where I believe we are:
>
> 1) No transcription errors were identified during a review of the
> reference envelope bioassay results.
> 2) The total biomass calculations were done correctly.
> 3) Mortality should be computed as test/control. This is consistent
> with Table 2-1 in the March 17, 2006 Bioassay Interpretation Report,
> ASTM Method E-1706, and EPA Guidance.
> 4) Duplicate reference envelope samples should be pooled (averaged)
> rather than treated as individual samples. This is consistent with
> February 15, 2008 problem formulation (Note: is this the correct
> reference? I could not find this in either the problem formulation nor
> the MacDonald benthic risk evaluation)
> 5) Identification of Level 1, Level 2 and Level 3 thresholds: The
> toxicity thresholds should be calculated based on 10% of the reference
> envelope not an absolute 10%. This is consistent with Tables RE 1, RE-2
> and the text of EPA's March 31, 2009 direction on the Calculation and
> Use of Reference Envelope for Portland Harbor Sediment Toxicity Test
> Interpretation
> 6) Identification of the 5% of the reference envelope should be
> accomplished using a range of curve fitting procedures appropriate for
> the data set distribution. The curve fitting procedure with the best
> overall fit should be selected and the 5% calculated using the best fit
> curve fitting procedure.
>
> The above procedures for computing the results of the bioassay tests,
> calculating hit/no-hit designations, developing the reference envelope
> and identifying Level 1, Level 2 and Level 3 toxicity hits should be
> followed.
>
> Please look this over and make sure it matches up with the recommended
> procedures. See also my note about the pooling of the reference
> duplicate samples. Once everyone agrees with the outlined procedures, I
> will send an email to the LWG summarizing this and recommending a
> conference call to discuss if there area any questions.
>
> Thanks, Eric
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